

Amendments to the Specification:

Please replace the title with the following rewritten title:

-- ~~Mammalian Cell Membrane Proteins; Related Reagents~~ MDL-1
POLYPEPTIDES--

Please replace the paragraph beginning at page 1, line 4, with the following rewritten paragraph:

-- This filing is a divisional of ~~co-pending application~~ USSN 10/191,732, filed July 8, 2002, now US Patent No. 6,953,843, which ~~claims benefit from a Divisional is a divisional~~ of USSN 09/127,946, filed July 31, 1998, now U.S. Patent No. 6,416,973, ~~issued July 9, 2002~~, which claims benefit of U.S. Provisional Patent Applications 60/089,168, filed June 12, 1998; 60/069,639, filed December 15, 1997; 60/063,717, filed October 29, 1997; 60/069,692, filed December 16, 1997; and 60/054,430, filed August 1, 1997; each of which is incorporated herein by reference. --

Please replace the paragraph beginning on page 3, line 17, with the following rewritten paragraph:

--Binding compounds are also provided, comprising an antigen binding portion from an antibody, which specifically binds to: a natural DAP12 polypeptide, wherein the antibody: is raised against a mature polypeptide of Table 1 SEQ ID NO:2 or 6; is immunoselected; is a polyclonal antibody; binds to a denatured DAP12; exhibits a Kd to antigen of at least 30 \square M; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label; or a natural DAP10 polypeptide, wherein the antibody: is raised against a mature polypeptide of Table 2 SEQ ID NO: 8 or 10; is immunoselected; is a polyclonal antibody; binds to a denatured DAP10; exhibits a Kd to antigen of at least 30 \square M; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile

composition; or is detectably labeled, including a radioactive or fluorescent label; or a natural MDL-1 polypeptide, wherein the antibody: is raised against a mature polypeptide of Table 3 SEQ ID NO: 12 or 14; is immunoselected; is a polyclonal antibody; binds to a denatured MDL-1; exhibits a Kd to antigen of at least 30 μ M; is attached to a solid substrate, including a bead or plastic membrane; is in a sterile composition; or is detectably labeled, including a radioactive or fluorescent label. Various kits are provided, e.g., comprising the binding compound, and: a compartment comprising the binding compound; and/or instructions for use or disposal of reagents in the kit. Additional embodiments include a composition comprising: a sterile binding compound, or the binding compound and a carrier, wherein the carrier is: an aqueous compound, including water, saline, and/or buffer; and/or formulated for oral, rectal, nasal, topical, or parenteral administration.--

Please replace the paragraph beginning on page 4, line 1, with the following rewritten paragraph:

-- Nucleic acid embodiments include an isolated or recombinant nucleic acid encoding these polypeptides, wherein the nucleic acid encodes an antigenic peptide sequence of ~~Table 1, 2, or 3~~ SEQ ID NO: 2, 6, 8, 10, 12, or 14. Preferred embodiments include such a nucleic acid, which encodes a plurality of antigenic peptide sequences of the table. Other nucleic acids include one which: is an expression vector; further comprises an origin of replication; is from a natural source; comprises a detectable label; comprises synthetic nucleotide sequence; is less than 6 kb, preferably less than 3 kb; is from a mammal, including a primate or rodent; comprises a natural full length coding sequence; is a hybridization probe for a gene encoding DAP12, DAP10, or MDL-1; or is a PCR primer, PCR product, or mutagenesis primer--

Please replace the paragraph beginning on page 7, line 17, with the following rewritten paragraph:

-- Table 1 discloses both the nucleotide sequence (SEQ ID NO: 1 and 5) of the cDNA and the corresponding amino acid sequence for DAP12 embodiments. The primate nucleotide sequence corresponds to SEQ ID NO: 1; the amino acid sequence corresponds to SEQ ID NO: 2. The signal sequence appears to run from met(-26) to gln(-1) or ala1; the mature protein should run from about ala1 (or gln2), the extracellular domain from about ala1 to pro14; the extracellular domain contains two cysteines at 7 and 9, which likely allow disulfide linkages to additional homotypic or heterotypic accessory proteins; the transmembrane region runs from about gly15 or val16 to about gly39; and an ITAM motif from tyr65 to leu79 (YxxL-6/8x-YxxL). The LVA03A EST was identified and used to extract other overlapping sequences. See also Genbank Human ESTs that are part of human DAP12; some, but not all, inclusive Genbank Accession # AA481924; H39980; W60940; N41026; R49793; W60864; W92376; H12338; T52100; AA480109; H12392; W74783; and T55959.--

Please replace the paragraph beginning on page 10, line 1, with the following rewritten paragraph:

-- Table 2 discloses both the nucleotide sequence of the cDNA and the corresponding amino acid sequence (SEQ ID NO: 7, 8, 9, and 10) of each of the human and mouse DAP10 genes. The nucleotide sequence for human corresponds to SEQ ID NO: 7; the amino acid sequence corresponds to SEQ ID NO: 8. The signal sequence appears to run from about met(-18) to ala(-1); the mature protein should run from about gln1, the extracellular domain from about gln1 to pro30; the extracellular domain contains two cysteines at 21 and 24, which likely allow disulfide linkages to additional homotypic or heterotypic accessory proteins; the transmembrane region runs from about leu31 to val47, with a characteristic charged residue corresponding to asp39; and an interesting YxxM motif from tyr67 to met70, which is similar to that seen in CD28, CTLA-4, and CD19. See Table 2.--

Please replace the paragraph on page 15, lines 13-17, with the following rewritten paragraph:

--Alignment of human MDL-1 (SEQ ID NO: 12) and mouse MDL-1 long form (SEQ ID NO: 14). Of particular interest are a very short intracellular domain, corresponding to residues 1-2; with the transmembrane domain running from about 6 to 27 possessing a charged amino acid at about residue 16. Three putative N-linked glycosylation sites correspond to residues 51, 146, and 153 of the mouse long form; the latter of which are conserved in the human sequence. Note that the mouse long form, relative to the short form, appears to contain a spacer segment of about 25 amino acids.--

Please replace the paragraph beginning on page 16, line 1, with the following rewritten paragraph:

-- As used herein, the term "human DAP12" shall refer, when used in a protein context, to a protein having the primate amino acid sequence shown in Table 1 of SEQ ID NO: 2. The present invention also encompasses proteins comprising a substantial fragment thereof, e.g., mutants and polymorphic variants, along with a human derived polypeptide which exhibits the same biological function or interacts with human DAP12 specific binding components. These binding components typically bind to a human DAP12 with high affinity, e.g., at least about 100 nM, usually better than about 30 nM, preferably better than about 10 nM, and more preferably at better than about 3 nM. Homologous proteins are found in species other than humans, e.g., primates. While most of the description below is directed to DAP12, similar methods and features may be analogously applicable to the DAP10 and MDL-1 genes. Many limitations directed to DAP12 will correspond to terms in reference to DAP10 and MDL-1, though specific limitations relevant to one gene, e.g., a length limitation, will not necessarily intended to apply to the others.--

Please replace the paragraph beginning on page 18, line 28, with the following rewritten paragraph:

-- The isolated human DAP and MDL DNA can be readily modified by nucleotide substitutions, nucleotide deletions, nucleotide insertions, and inversions of nucleotide stretches. These modifications will result in novel DNA sequences which encode useful antigens, their derivatives, or proteins having similar or antagonist activity. These modified sequences can be used to produce mutant antigens or to enhance expression. Enhanced expression may involve gene amplification, increased transcription, increased translation, and other mechanisms. Such mutant DAP12 derivatives include predetermined or site-specific mutations of the respective protein or its fragments. "Mutant DAP12" encompasses a polypeptide otherwise sharing important features of the human DAP12 as set forth above, but having an amino acid sequence which differs from that of DAP12 as found in nature, whether by way of deletion, substitution, or insertion. In particular, "site specific mutant DAP12" is defined as having homology with an antigen of Table 4 SEQ ID NO: 2, and as sharing relevant biological activities with those antigens. Similar concepts apply to different DAP12 proteins, particularly those found in various other mammals. As stated before, it is emphasized that descriptions are generally meant to encompass additional DAP and MDL proteins, not limited solely to the primate embodiment specifically discussed.--

Please replace the paragraph beginning on page 22, line 27, through page 23, line 7, with the following rewritten paragraph:

-- A solubilized DAP or MDL antigen of this invention can be used as an immunogen for the production of antisera or antibodies specific for the antigen or many fragments thereof. The purified antigens can be used to screen monoclonal antibodies or antigen-binding fragments prepared by immunization with various forms of impure preparations containing the protein. In particular, the term "antibodies" also encompasses antigen binding fragments of natural antibodies. The purified DAP or MDL can also be used as a reagent to detect antibodies generated in response to the presence of elevated levels of DAP, MDL, or cell fragments containing the antigen, both of which may be diagnostic of an abnormal or specific physiological or disease condition. Additionally, DAP or MDL fragments may also serve as immunogens to

produce the antibodies of the present invention, as described immediately below. For example, this invention contemplates antibodies raised against amino acid sequences of, or encoded by nucleotide sequences ~~shown in, e.g., Table 1, 2, or 3, of SEQ ID NOs: 1-14~~ or fragments thereof. In particular, this invention contemplates antibodies having binding affinity to or being raised against specific fragments which are predicted to lie outside of the lipid bilayer, either extracellular or intracellular domains. Additionally, various constructs may be produced from fusion of a membrane associating segment to the otherwise extracellular exposed portion of the molecule. Other antigenic complexes may be used, including complexes of the DAP or MDL with a receptor partner.--

Please replace the paragraph beginning on page 28, line 5, with the following rewritten paragraph:

-- This invention contemplates use of isolated DNA or fragments to encode, e.g., a biologically active corresponding DAP12 polypeptide. In addition, this invention covers isolated or recombinant DNA which encodes a biologically active protein or polypeptide which is capable of hybridizing under appropriate conditions with the DNA sequences described herein. Said biologically active protein or polypeptide can be an intact DAP12, or fragment, and have an amino acid sequence encoded by a nucleic acid ~~shown in Table 4 of SEQ ID NO: 1 or 5~~. Further, this invention covers the use of isolated or recombinant DNA, or fragments thereof, which encodes a protein which is homologous to a DAP12 or which was isolated using cDNA encoding human DAP12 as a PCR or hybridization probe. The isolated DNA can have the respective regulatory sequences in the 5' and 3' flanks, e.g., promoters, enhancers, poly-A addition signals, and others.--

Please replace the paragraph beginning on page 31, line 36, with the following rewritten paragraph:

--Substantial identity in the nucleic acid sequence comparison context means either that the segments, or their complementary strands, when compared, are identical when optimally aligned, with appropriate nucleotide insertions or deletions, in at least about 50% of the nucleotides, generally at least about 56%, more generally at least about 59%, ordinarily at least about 62%, more ordinarily at least about 65%, often at least about 68%, more often at least about 71%, typically at least about 74%, more typically at least about 77%, usually at least about 80%, more usually at least about 85%, preferably at least about 90%, more preferably at least about 95 to 98% or more, and in particular embodiments, as high at about 99% or more of the nucleotides. Alternatively, substantial identity exists when the segments will hybridize under selective hybridization conditions, to a strand, or its complement, typically using a sequence ~~derived from Table 4 of SEQ ID NO: 1 or 5.~~ Typically, selective hybridization will occur when there is at least about 55% homology over a stretch of at least about 14 nucleotides, preferably at least about 65%, more preferably at least about 75%, and most preferably at least about 90%. See, Kanehisa (1984) Nuc. Acids Res. 12:203-213. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will be over a stretch of at least about 17 nucleotides, usually at least about 20 nucleotides, more usually at least about 24 nucleotides, typically at least about 28 nucleotides, more typically at least about 40 nucleotides, preferably at least about 50 nucleotides, and more preferably at least about 75 to 100 or more nucleotides, e.g., 125, 150, 200, 250, 300, etc.--

Please replace the paragraph beginning on page 48, line 3, with the following rewritten paragraph:

-- Two primers are designed according to the provided sequences. To increase the chances of obtaining PCR products, human THP-1 cells, Th1 T cells, monocytes activated with LPS, IFN- γ and IL-10, or NK cells are used. A product is purified, subcloned into pCRTM vector (Invitrogen, San Diego CA), and then sequenced. See Tables 1, 2, and 3 SEQ ID NO: 1, 2, 5, 6, 7, 8, 9, 10, 11, 12, 13, and 14.--

Please replace the paragraph beginning on page 48, line 35, with the following rewritten paragraph:

--~~Tables 1, 2, and 3 sequences~~ SEQ ID NO: 5, 9, and 13 allow design of a probe or primer which will allow isolation of mouse counterparts. With the primate and rodent sequences, other species counterparts can be identified using conserved sequences, either nucleic acid or epitopes.--